

VIA FIRST CLASS MAIL

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FULBRIGHT & JAWORSKI L.P.

By

Norman D. Hanson

LUD 5615 (09905230)

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TECH CENTER 1600/2900

P#13

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) : JAGER, et al.

Serial No. : 09/451,739

Filed : November 30, 1999

For : ISOLATED NUCLEIC ACID MOLECULES ENCODING
CANCER ASSOCIATED ANTIGENS, THE ANTIGENS
PER SE, AND USES THEREOF

Group Art Unit : 1642

Examiner : G. Nickol

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Hon. Commissioner of Patents
and Trademarks
Washington, D.C. 20231

February 2, 2001

LETTER

In response to the office action of January 28, please replace the paper copy of the sequence listing and CRF of same with the attached.

The undersigned hereby declares that to the best of his knowledge, the information presented on the attached paper copy of sequence listing and computer readable form thereof are identical to each other and to information set forth in the above referenced patent application as filed. No new matter is believed presented.

Respectfully submitted,

FULBRIGHT & JAWORSKI L.P.

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666 Fifth Avenue
New York, New York 10103
(212) 318-3000

<110> Jager, Dirk
Scanlan, Matthew
Gure, Ali
Jager, Elke
Knuth, Alexander
Old, Lloyd
Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
the Antigens per se, and Uses Thereof

<130> LUD 5615

<140> 09/451,739

<141> 1999-11-30

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Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg
260 265 270

Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys
275 280 285

Glu Arg Ala Tyr Asn Arg
290 294

**UNITED STATES DEPARTMENT OF COMMERCE****Patent and Trademark Office**

Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

13

APPLICATION NO.	PROMINATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/451,739	11/30/99	JAGER	140-5615

024972
FULBRIGHT & JAWORSKI, LLP
666 FIFTH AVE
NEW YORK NY 10103-3198

HMK2270130

EXAMINER

WICKES, JR.

ART UNIT

PAPER NUMBER

1642

DATE MAILED:

01/20/01

Please find below and/or attached an Office communication concerning this application or proceeding.

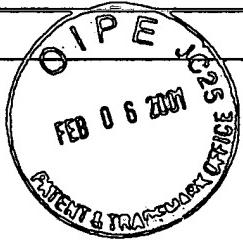
Commissioner of Patents and TrademarksDOCKET SHEET
FEB 1 2001

FULBRIGHT & JAWORSKI, LLP
NEW YORK DOCKETING
Docketed Not Required
Previously Updated
Docket No: 140-5615 | NDH
Action: Sequence listing
Reminder: 2/21/2001
Date Due/Done: 2/28/2001
Initials: (LJ)

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

DEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/451739			



EXAMINER	
Gary B. Nickol Ph.D.	
ART UNIT	PAPER NUMBER
1642	

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication filed on 01/02/01 is not fully responsive for the reasons set forth on the attached Notice to Comply with the Sequence Rules or CRF Diskette Problem Report.

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.136 (g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gary Nickol, Ph.D. whose telephone number is (703) 305-7143. The examiner can normally be reached on Monday through Friday from 830am to 630pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, can be reached on (703) 308-3995. The fax phone number for this Group is (703) 305-3014 or (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

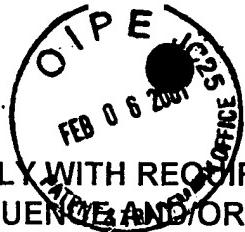
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FEB 13 2001

Gary B. Nickol Ph.D.
January 26, 2001

AM
ANTHONY C. CAPUTA
EXAMINER
TECH CENTER 1600
U.S. PATENT & TRADEMARK OFFICE

TECH CENTER 1600/2000



Application No.: 09/451739

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCES AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: _____

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Applicant Must Provide:

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- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

BIOTECH
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:



Application Serial Number: 09/451,739B

Source: 1642

Date Processed by STIC: 1/2/2001

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/451,739B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|---|---|
| 1 | Wrapped Nucleic

Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 4 | Incorrect Line Length | The amino acid number/text at the end of each line "wrapped", down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 5 | Misaligned Amino Acid Numbering | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 6 | Non-ASCII | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 7 | Variable Length | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 8 | PatentIn ver. 2.0 "bug" | Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 9 | Skipped Sequences (OLD RULES) | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 10 | Skipped Sequences (NEW RULES) | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 11 | Use of n's or Xaa's (NEW RULES) | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 12 | Use of <213>Organism (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 13 | Use of <220>Feature (NEW RULES) | Sequence(s) _____ are missing this mandatory field or its response. |
| | PatentIn ver. 2.0 "bug" | Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| | PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |

1642



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001
TIME: 11:02:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\01022001\I451739B.raw

Does Not Comply
Corrected Diskette Needed

see item 5 on
Error
summary
sheet

ERRORED SEQUENCES

520 <210> SEQ ID NO: 16
 521 <211> LENGTH: 513
 522 <212> TYPE: PPT
 523 <213> ORGANISM: Homo sapiens
 OK-> 524 <400> SEQUENCE: 16
 525 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Ser Met Asp Met Gln
 526 1 6 10 15
 527 Thr Phe Lys Ala Glu Pro Pro Gln I/S Pro Ser Ala Phe Glu Pro Ala
 528 20 25 30
 529 Ile Glu Met Glu Lys Ser Val Pro Asn Lys Ala Leu Glu Ile Lys Asn
 530 35 40 45
 531 Glu Glu Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Gln Ser Iys Gln
 532 50 55 60
 533 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
 534 65 70 75 80
 535 Val Ser Glu Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Iys Glu
 536 85 90 95
 537 Ile Asp Lys Ile Asn Gly Iys Leu Glu Ser Pro Asp Asn Asp Gly
 538 100 105 110
 539 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Iys Ala
 540 115 120 125
 541 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Gln Lys
 542 130 135 140
 543 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
 544 145 150 155 160
 545 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
 546 165 170 175
 547 Phe Pro Ser Glu Ser Lys Gln Lys Val Glu Glu Asn Ser Trp Asp
 548 180 185 190

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001

TIME: 11:02:39

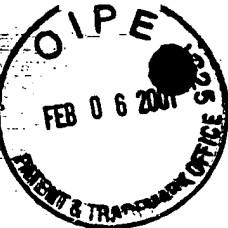
Input Set : A:\ES.txt

Output Set: N:\Crf3\01022001\I451739B.raw

562 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
 563 195 200 205
 565 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
 566 210 215 220
 568 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
 569 225 230 235 240
 571 Arg Ala Arg Glu Leu Gin Lys Asp His Cys Glu Gln Arg Thr Gin Lys
 E--> 572 245 250 255
 574 Met Gin Gln Met Lys Lys Lys Lys Gin Val Leu Lys Lys Lys Leu Ser
 E--> 575 260 265 270 275
 577 Gin Ala Lys Glu Ile Lys Ser Gin Leu Glu Asn Gln Lys Val Lys Ile
 E--> 578 275 280 285
 580 Glu Gin Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Glu Gln Glu Glu
 E-> 581 280 295 300 305
 583 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
 E--> 584 310 315 320
 586 Gly Arg Ile Glu Glu Gln His Arg Ile Glu Leu Glu Val Lys Gln Glu
 E--> 587 325 330 335
 589 Leu Glu Gln Ala Leu Arg Ile Ile Asp Ile Glu Leu Lys Leu Val Glu
 E--> 590 340 345 350
 592 Ser Asn Leu Asn Gln Val Ser His Ile His Glu Asn Glu Asn Tyr Leu
 E--> 593 355 360 365
 595 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
 E--> 596 370 375 380 385
 598 Glu Ile Ala Thr Leu Lys His Ile Ile Glu Glu Lys Glu Asn Lys Tyr
 E--> 599 390 395 400
 601 Phe Glu Asp Ile Lys Ile Leu Ile Glu Lys Asp Ala Glu Leu Glu His
 E--> 602 405 410 415
 604 Thr Leu Lys Leu Lys Glu Glu Ser Ile Thr Lys Arg Ala Ser Glu Tyr
 E--> 605 420 425 430
 607 Ser Gln Glu Leu Lys Val Leu Ile Ala His Asn Thr Met Leu Thr Ser
 E--> 608 435 440 445
 619 Lys Leu Lys Glu Lys Glu Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
 E--> 611 450 455 460 465
 613 Ser His His Pro Arg Leu Ala Ser Ala Val Glu Asp His Asp Glu Ile
 E--> 615 470 475 480
 617 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Glu Asp
 E--> 618 485 490 495
 620 Ala Cys Leu Glu Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
 E--> 621 500 505 510

misaligned amino acid numbers
 (see item 4 on Error Summary sheet)

All next page for more errors



09/451,739B

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<210> 1
<211> 1533
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 235
<400> 1
ggttttccac gttggacaag tgcggctcg ggccagcgg agcgccccc ttcccgtgc 60
ccgctccgct cctcttctt acccagccca gtggcgagt gggcagcggc ggccgcggcg 120
ctggccctc tccccccggt gtgtgcgc tcgtacgcgc ggcggccggc gccagccccc 180
ccgcctgaga gggggcctgc gcccggcc gggcgtgcg cccgggagcc accccccccg 240
cggcccgccg cctcaggcgc tgggtcccc gcggaccgg aggccggcga cggctcggc 300
agatgtagec gccccggcga agcaggagcc ggcggggggg cgccgggaga gcgagggttt 360
tgcatttgc agtgctattt tttgaggggg gcggagggtg gaggaagtgc gaaagccgcg 420
ccgagtcgcc ggggacctcc ggggtgaacc atgtttagtc ctgccaacgg ggacgagctc 480
cacctggta actatgtgaa ggactacctg gactccatcg agtccctgcc ttccgtactt 540
cagagaaatg tctcgctgat gcgggagatc gacgcgaaat accaagagat cctgaaggag 600
ctagacgagt gctacgagcg cttcagtcgc gagacagacg gggcgcagaa gcggcggatg 660
ctgcactgtg tgcagcgcgc gctgatccgc agccaggagc tggcgcacga gaagatccag 720
atcgtgagcc agatggtgaa gctgggtggag aaccgcacgc ggcaggtgga cagccacgtg 780
gagctgtcg aggccgcagca ggagctggc gacacagcgg gcaacagcgg caaggctggc 840
gcggacaggc ccaaaggcga ggcggcagcg caggctgaca agcccaacag caagcgctca 900
cggccgcagc gcaacaacga gaaccgtgag aacgcgtcca gcaaccacga ccacgacgac 960
ggcgcctcg gCACACCCAA ggagaagaag gccaagaccc ccaagaagaa gaagcgctcc 1020
aaggccaagg cggagcgaga ggcgtccct gcccacctcc ccatcgaccc caacgaaccc 1080
acgtactgtc tgtgcaacca ggtctccat gggagatga tcggctgcga caacgacgag 1140
tgccccatcg agtggttcca cttctcggtc gtggggctca atcataaacc caaggcaag 1200
tggactgtc ccaagtgcgg gggggagaac gagaagacca tggacaaagc cctggagaaa 1260
tccaaaaaag agagggctta caacaggtag tttgtggaca ggcgcctggt gtgaggagga 1320
caaaataaac cgtgtattta ttacattgtc gccttggtg aggtgcaagg agtgtaaaat 1380
gtatatttt aaagaatgtt agaaaaggaa ccattcctt catagggatg gcagtgattc 1440
tggttgcctt ttgtttcat tggtacacgt gtaacaagaa agtggtctgt ggatcagcat 1500
tttagaaaact acaaataatag gtttgattca aca 1533

? see
item 10
in Error
Summary Sheet

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US2001/451,739

DATE: 01/02/2001

TIME: 11:02:40

Input Set : A:\ES.txt
Output Set: N:\Crf3\01022001\I451739B.raw

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L:26 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#1
L:36 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#1
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:265 M:283 W: Missing Blank Line separator, <400> field identifier
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:367 M:283 W: Missing Blank Line separator, <400> field identifier
L:390 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#8
L:390 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#8
L:490 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#8
L:399 M:283 W: Missing Blank Line separator, <400> field identifier
L:407 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:283 W: Missing Blank Line separator, <400> field identifier
L:423 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:283 W: Missing Blank Line separator, <400> field identifier
L:450 M:283 W: Missing Blank Line separator, <400> field identifier
L:503 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#15
L:503 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#15
L:505 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#15
L:509 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#15
L:509 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#15
M:340 Repeated in SeqNo 14
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#15
L:513 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#15
L:515 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#15
L:515 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#15
L:517 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#15
L:517 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#15
L:524 M:283 W: Missing Blank Line separator, <400> field identifier
L:572 M:342 E: (32) Invalid/Missing Amino Acid Numbering: SEQ ID#16
M:332 Repeated in SeqNo 15
L:621 M:252 E: No. of Seq. differs. 311<451>:Input:513 Found:512 Seq:16
L:628 M:283 W: Missing Blank Line separator, <400> field identifier
L:636 M:283 W: Missing Blank Line separator, <400> field identifier
L:644 M:283 W: Missing Blank Line separator, <400> field identifier